	SEQUENCE LISTING											
<110>	Lee, Richar Landschulz, Turi, Thoma Thompson, S Kennedy, So	. Katherine as G. John F.	т.	Title: DIAGNOS	gned AUGUST 21, 2001 S AND TREATMENT OF LAR CONDITIONS							
<120>	DIAGNOSIS A	AND TREATMEN	T OF CARDI	OVASCULAR CONDITI	ONS							
<130>	P0738/7001,	/ERP/KA										
	US 60/227,1	159										
<160>	17											
<170>	FastSEQ for	Windows Ve	rsion 3.0									
<212>	1321	ns										
	CDS (413)(12	273)										
cggcggcggc ggcggcagcg acgcccccgg tgagccccgc	cteggagega a ggeggeggag g egegeeeege t ggetgeeegg g ggegeeeegg g	gegetegget g gecagecea t gggaggeegg g gaaettggeg g geatgeggg g	gggaaaget a ttteeggae a ggggegeag a egaeeegag a eeeeagete a	gaatgaggag gaggac agcggcagag gctcac gccaccogcg ggcact cggagcgcgg tcccgc cccggcgagc cgggc ggggcgccgg ccggac gccgcgccgt cc atc Mct	cccc 120 gccg 180 gcac 240 gcgc 300 cccc 360							
cgc ttg atg Arg Leu Met 5	ggg gtc aac Gly Val Asr	e age ace ge n Ser Thr Al 10	c gcc gcc o a Ala Ala i	gee gee ggg eag e Ala Ala Gly Gln F 15	ro 466							
				etg tto cag ago a Leu Phe Gln Ser M 30								
		1 Phe Val Gl		atc atc gtg gtg g Ile Ile Val Val V								
				ctg agc cac tac a Leu Ser His Tyr I 65								
ctg tct gca Leu Ser Ala	cgg tcc ttc Arg Ser Phe 70	c atc agc cg e Ile Ser Ar 7	g His Ser (cag ggg cgg agg a Gln Gly Arg Arg A 80	ga 658 rg							

gaa gat gcc ctg tcc tca gaa gga tgc ctg tgg ccc tcg gag agc aca Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu Ser Thr

706

90

TOPUSTURO TOBELLA

95

						atc Ile											754	
	ccc Pro 115	acc Thr	gac Asp	ege Arg	ctg Leu	gcc Ala 120	gtg Val	ccg Pro	ccc Pro	ttc Phe	gcc Ala 125	cag Gln	cgg Arg	gag Glu	cgc Arg	ttc Phe 130	802	
						acc Thr											850	
I	cca Pro	ccc Pro	acc Thr	atc Ile 150	tcg Ser	ctg Leu	tca Ser	gac Asp	ggg Gly 155	gag Glu	gag Glu	ccc Pro	cca Pro	ccc Pro 160	tac Tyr	cag Gln	898	
						cag Gln											946	
ì	aac Asn	cgg Arg 180	gag Glu	tcg Ser	gtg Val	cgc Arg	gca Ala 185	ccc Pro	cca Pro	aac Asn	aga Arg	acc Thr 190	atc Ile	ttc Phe	gac Asp	agt Ser	994	
1	gac Asp 195	ctg Leu	atg Met	gat Asp	agt Ser	gcc Ala 200	agg Arg	ctg Leu	ggc Gly	ggc Gly	ccc Pro 205	tgc Cys	ccc Pro	ccc Pro	agc Ser	agt Ser 210	1042	
ì	aac Asn	tcg Ser	ggc Gly	atc Ile	agc Ser 215	gcc Ala	acg Thr	tgc Cys	tac Tyr	ggc Gly 220	agc Ser	ggc Gly	ggg Gly	cgc Arg	atg Met 225	gag Glu	1090	
Ċ	ggg Gly	ccg Pro	ccg Pro	ccc Pro 230	acc Thr	tac Tyr	agc Ser	gag Glu	gtc Val 235	atc Ile	ggc Gly	cac His	tac Tyr	ccg Pro 240	ggg Gly	tcc Ser	1138	
ţ	ec Ser	ttc Phe	cag Gln 245	cac His	cag Gln	cag Gln	agc Ser	agt Ser 250	ggg Gly	ccg Pro	ccc Pro	tcc Ser	ttg Leu 255	ctg Leu	gag Glu	gly ggg	1186	
						aca Thr											1234	
7	gg rp 275	agc Ser	aaa Lys	gag Glu	aag Lys	gat Asp 280	aaa Lys	cag Gln	aaa Lys	gga Gly	cac His 285	cct Pro	ctc Leu	tago	gted	ec	1283	
õ	iggç	gggc	eg g	getç	gggd	et go	gtag	gtga	aaa	iggea	ıg						1321	
		<2 <2	210> 211> 212> 213>	287 PRT	Sar	oiens												
ŀ	ſet		00> Arg		Met	G1v	Val	Asn	Ser	Thr	Ala	Ala	Ala	Ala	Ala	Glv		

Met His Arg Leu Met Gly Val Asn Ser Thr Ala Ala Ala Ala Ala Gly 1 Sin Pro Asn Val Ser Cys Thr Cys Asn Cys Lys Arg Ser Leu Phe Gln

```
20
                                25
Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Ile Ile Val
                            4.0
Val Val Met Met Val Met Val Val Val Ile Thr Cys Leu Leu Ser His
                        55
Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Gly Arg
                    70
                                        75
Arg Arg Glu Asp Ala Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser Glu
               85
Ser Thr Val Ser Gly Asn Gly Ile Pro Glu Pro Gln Val Tyr Ala Pro
                                105
                                                    110
Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ala Gln Arg Glu
                            120
                                                125
Arg Phe His Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile
                        135
                                            140
Asp Leu Pro Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro
                    150
                                        155
Tyr Gln Gly Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu
                165
                                    170
                                                        175
Glu Leu Asn Arg Glu Ser Val Arg Ala Pro Pro Asn Arg Thr Ile Phe
            180
                                185
                                                    190
Asp Ser Asp Leu Met Asp Ser Ala Arg Leu Gly Gly Pro Cys Pro Pro
       195
                            200
                                                205
Ser Ser Asn Ser Gly Ile Ser Ala Thr Cys Tyr Gly Ser Gly Gly Arg
                        215
Met Glu Gly Pro Pro Pro Thr Tyr Ser Glu Val Ile Gly His Tyr Pro
                    230
                                        235
                                                            240
Gly Ser Ser Phe Gln His Gln Gln Ser Ser Gly Pro Pro Ser Leu Leu
                245
                                    250
                                                        255
Glu Gly Thr Arg Leu His His Thr His Ile Ala Pro Leu Glu Ser Ala
            260
                                265
Ala Ile Trp Ser Lys Glu Lys Asp Lys Gln Lys Gly His Pro Leu
                            280
     <210> 3
     <211> 861
     <212> DNA
```

<213> Homo Sapiens

<220> <221> CDS

<222> (1)...(861)

<400> 3

atgcaccgct tgatgggggt caacagcacc gccgccgccg ccgccgggca gcccaatgtc teetgeaegt gcaactgcaa acgetetttg tteeagagca tggagateae ggagetggag tttgttcaga tcatcatcat cgtggtggtg atgatggtga tggtggtggt gatcacgtgc etgetgagee actacaaget gtetgeaegg teetteatea geeggeaeag eeaggggegg aggagagaag atgccctgtc ctcagaagga tgcctgtggc cctcggagag cacagtgtca ggcaacggaa teccagagee geaggtetac geecegeete ggeecacega cegeetggee gtgccgccct tcgcccagcg ggagcgcttc caccgcttcc agcccaccta tccgtacctg cagcacgaga tegacetgee acceaccate tegetgteag acggggagga gececcacce taccagggcc cctgcaccct ccagcttegg gaccccgagc agcagctgga actgaaccgg gagteggtge gegeaccece aaacagaace atettegaca gtgacetgat ggatagtgee aggotgggeg geccetgece ecceageagt aactegggea teagegeeae gtgetaegge agoggoggo goatggaggg googcogcoc acctacagog aggtcatogg coactacoog gggtcctcct tccagcacca gcagagcagt gggccgccct ccttgctqqa gqqqacccqq ctccaccaca cacacatege geceetagag agegeageca tetggageaa agagaaggat aaacagaaag gacaccctct c

60

180

240

300

360

420

480

540

720

780

840

861

```
<211> 477
      <212> DNA
      <213> Homo Sapiens
      <220>
      <221> CDS
      <222> (7)...(474)
      <223> IEX1
      <400> 4
ctcacc atg tgt cac tct cgc agc tgc cae ccg acc atg acc atc ctg
                                                                      4.8
      Met Cys His Ser Arg Ser Cys His Pro Thr Met Thr Ile Leu
cag gee eeg ace eeg gee eee tee ace ate eeg gga eee egg egg gge
                                                                      96
Gln Ala Pro Thr Pro Ala Pro Ser Thr Ile Pro Gly Pro Arg Arg Gly
tee ggt eet gag ate tte ace tte gae eet ete eeg gag eee gea geg
                                                                     144
Ser Gly Pro Glu Ile Phe Thr Phe Asp Pro Leu Pro Glu Pro Ala Ala
                                     40
gce cet gee ggg ege eee age gee tet ege ggg eac ega aag ege age
                                                                     192
Ala Pro Ala Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser
ege agg gtt ete tae eet ega gtg gte egg ege eag etg eea gte qag
                                                                     240
Arg Arg Val Leu Tyr Pro Arg Val Val Arg Arg Gln Leu Pro Val Glu
gaa cog aac coa god aaa agg ott oto ttt otg otg oto acc atc gto
Glu Pro Asn Pro Ala Lys Arg Leu Leu Phe Leu Leu Leu Thr Ile Val
ttc tgc cag atc ctg atg gct gaa gag ggt gtg ccg gcg ccc ctg cct
                                                                     336
Phe Cys Gln Ile Leu Met Ala Glu Glu Gly Val Pro Ala Pro Leu Pro
                    100
                                        105
cca gag gac gcc cet aac gcc gca tcc ctg gcg ccc acc cct gtg tcc
                                                                     384
Pro Glu Asp Ala Pro Asn Ala Ala Ser Leu Ala Pro Thr Pro Val Ser
ccc gtc ctc gag ccc ttt aat ctg act tcg gag ccc tcg gac tac gct
                                                                     432
Pro Val Leu Glu Pro Phe Asn Leu Thr Ser Glu Pro Ser Asp Tyr Ala
                                135
ctg gac etc age act tte etc cag caa cae eeg gee gee tte
                                                                     474
Leu Asp Leu Ser Thr Phe Leu Gln Gln His Pro Ala Ala Phe
                            150
taa
                                                                     477
      <210> 5
      <211> 156
      <212> PRT
      <213> Homo Sapiens
     <400> 5
Met Cys His Ser Arg Ser Cys His Pro Thr Met Thr Ile Leu Gln Ala
                5
                               10 15
```

Pro Thr Pro Ala Pro Ser Thr Ile Pro Gly Pro Arg Arg Gly Ser Gly

									-3-							
Pro	Glu	Ile	20 Phe	Thr	Phe	Asp		25 Leu	Pro	Glu	Pro		30 Ala	Ala	Pro	
Ala		35 Arg	Pro	Ser	Ala		40 Arg	Gly	His	Arg		45 Arg	Ser	Arg	Arg	
	50 Leu	Tyr	Pro	Arg		55 Val	Arg	Arg	Gln		60 Pro	Val	Glu	Glu		
65 Asn	Pro	Ala	Lys		70 Leu	Leu	Phe	Leu		75 Leu	Thr	Ile	Val		80 Cys	
Gln	Ile	Leu	Met	85 Ala	Glu	Glu	Gly	Val	90 Pro	Ala	Pro	Leu	Pro	95 Pro	Glu	
Asp	Ala	Pro		Ala	Ala	Ser	Leu 120		Pro	Thr	Pro	Val 125		Pro	Val	
Leu	Glu 130	Pro	Phe	Asn	Leu	Thr 135		Glu	Pro	Ser	Asp 140		Ala	Leu	Asp	
Leu 145		Thr	Phe	Leu	Gln 150		His	Pro	Ala	Ala 155						
	<2 <2	210> 211> 212> 213>	2704 DNA		oiens	3										
	<2 <2	220> 221> 222> 223>	(222		. (139	94)										
atto	agto catto taaaq	gt t	accaç taaa aata	itctt attt	a tt	ttat	tttt aagg	aaq g gtt	getea	aaac cga	tgct tttc c at	staa ggage sg g et Va	gaa 1 ott 1 og a1	acci ttti ig ti	gttaat ttaatt sttott sc aag ne Lys 5	60 120 180 236
		aag Lys														284
		ggc Gly														332
		cgt Arg 40														380
		tgg Trp														428
		tat Tyr														476
		atg Met														524
ggc	ttt	gag	ctt	cct	cag	ggg	cct	ctg	gga	aca	tee	ttc	aaa	gga	aaa	572

									-6-							
Gly	Phe	Glu	Leu 105	Pro	Gln	Gly	Pro	Leu 110	Gly	Thr	Ser	Phe	Lys 115	Gly	Lys	
					tac Tyr											620
					aca Thr											668
					gat Asp 155											716
					atg Met											764
					aaa Lys											812
					aat Asn											860
					cac His											908
					tca Ser 235											956
					cgt Arg											1004
					tgc Cys											1052
					cct Pro											1100
					aga Arg											1148
					tet Ser 315											1196
					cct Pro											1244
					cca Pro											1292

	345	350		355	
	Ser Pro Ile			ttc aag ttc Phe Lys Phe 370	
				ctc aac aac Leu Asn Asn	
gtg cag tga Val Gln 390	gcatgtg gaag	aaaaga agcag	cttta cctact	tgtt tottttt	gtc 1444
caccttagoc aaggatgogg gggtttaaaa tgaggoctt ggttttttgg atgtggagaa ttttggagaa ttttggagaaa gaaaaacctt aaaggaagtagt tgttctccta ggaattggtt ccttctgcca aagacaaaaa aacgcttaaa caaggaggaa tgagaatggt atgagaacata agagaatagg catagacatag catagacacct attacagcca 210 211	totgacttoe to actoatocto a ataactagaa a togatagttt o gagocttttg tagaccaatt a gagoggttott a ctagagotga totaagotga totaagotga totaagotga totaagotga totaaagotga totaaagotga totaaagotga totaaagotga totaaagotga totaagotgaagotg tagatattgga gaatattgga gaatattgga gaatattgga gaagotga totaagotga totaagotga gaagotga gaatattga a gaagotga gaatattga a gaagotga gaatattga a gaagotga gaatatga aagotga gaatatga gaaagotga gaatatga gaagotga gaaagotga gaagotga gaagotga gaaagotga gaagotga gaagot	aatdtagga gg gcoagogoc ox aactoaggo ox gaattgtga ta aaattgtga ta caaaactag ga aaatcagtg ti titgatggac aat ggaaaaggtot ta tictataga ga titettagaa tg titttagaa tg gattgatge tgi gattgocaa ox ticaataaa go ticaataaa go	tggtcagc agg tgtgtggg tac tatccattt tct taaatggc tcc ggaactt gga agatgaa agg tcccctt gtg tggaaga gct tttagaagag gct tttagatggt tta aaaagccat ttt ggatggt tta tcaattcc tgt gtctaactg tgt tccactg tgt tccactg tgt tccactg tgt tccacac gda tccacac gac tccacac gac tccacacac tgcacacac tccacacacac tccacacacacac tccacacaca	toaatgg agtg caatotc ctgg aggggtg tttg aggact cott tggcgta aggact tttgccttaga ctta agaattg tggc cacttgt agaa ttccttaa ctggtgagac tatt tctcat gtgtgagac tatt acaattt tttgcttagagcat atatt acagaatt atatt acctcag gatgagt actt	goetta 1564 tttggat 1624 gaaaat 1684 ttttcaa 1684 ttttcaa 1804 aaaaac 1864 aaaaac 1864 tattaaa 1984 cttttta 2044 gractt 2164 gractt 2164 gractt 224 gracaa 2284 aattec 2344 caaaac 2404 tttgcac 2464 tttgggtt 2524 ttcag 2584
1	Phe Lys Lys 5 Val Tyr Gly	Ser Gly Glu	10	Val Phe Asn 15 Gly Arg Val	•
	20	25		30	

Val Glu Val Cys Glu Val Thr Arg Val Lys Ala Val Arg Ile Leu Ala 45 40 Cys Gly Val Ala Lys Val Leu Trp Met Gln Gly Ser Gln Gln Cys Lys 50 55 60 Gln Thr Ser Glu Tyr Leu Arg Tyr Glu Asp Thr Leu Leu Leu Glu Asp 65 70 75 80Gln Pro Thr Gly Glu Asn Glu Met Val Ile Met Arg Pro Gly Asn Lys 85 90 95 Ser Phe Lys Gly Lys Tyr Gly Cys Val Asp Tyr Trp Val Lys Ala Phe 115 120 125 Leu Asp Arg Pro Ser Gln Pro Thr Gln Glu Thr Lys Lys Asn Phe Glu 130 135 140

Val Val Asp Leu Val Asp Val Asn Thr Pro Asp Leu Met Ala Pro Val

								-8-							
145				150					155					160	
Ser Ala	Lys	Lys	Glu 165	Lys	Lys	Val	Ser	Cys 170	Met	Phe	Ile	Pro	Asp 175	Gly	
Arg Val	Ser	Val 180	Ser	Ala	Arg	Ile	Asp 185	Arg	Lys	Gly	Phe	Cys 190	Glu	Gly	
Asp Glu	Ile 195	Ser	Ile	His	Ala	Asp 200	Phe	Glu	Asn	Thr	Cys 205	Ser	Arg	Ile	
Val Val 210	Pro	Lys	Ala	Ala	Ile 215	Val	Ala	Arg	His	Thr 220	Tyr	Leu	Ala	Asn	
Gly Gln 225	Thr	Lys	Val	Leu 230	Thr	Gln	Lys	Leu	Ser 235	Ser	Val	Arg	Gly	Asn 240	
His Ile	Ile	Ser	Gly 245	Thr	Cys	Ala	Ser	Trp 250	Arg	Gly	Lys	Ser	Leu 255	Arg	
Val Gln	Lys	Ile 260	Arg	Pro	Ser	Ile	Leu 265	Gly	Cys	Asn	Ile	Leu 270	Arg	Val	
Glu Tyr	Ser 275	Leu	Leu	Ile	Tyr	Val 280	Ser	Val	Pro	Gly	Ser 285	Lys	Lys	Val	
Ile Leu 290	Asp	Leu	Pro	Leu	Val 295	Ile	Gly	Ser	Arg	Ser 300	Gly	Leu	Ser	Ser	
Arg Thr 305	Ser	Ser	Met	Ala 310	Ser	Arg	Thr	Ser	Ser 315	Glu	Met	Ser	Trp	Val 320	
Asp Leu	Asn	Ile	Pro 325	Asp	Thr	Pro	Glu	Ala 330	Pro	Pro	Cys	Tyr	Met 335	Asp	
Val Ile	Pro	Glu 340	Asp	His	Arg	Leu	Glu 345	Ser	Pro	Thr	Thr	Pro 350	Leu	Leu	
Asp Asp	Met 355	Asp	Gly	Ser	Gln	Asp 360	Ser	Pro	Ile	Phe	Met 365	Tyr	Ala	Pro	
Glu Phe 370	Lys	Phe	Met	Pro	Pro 375	Pro	Thr	Tyr	Thr	Glu 380	Val	Asp	Pro	Cys	
Ile Leu 385	Asn	Asn	Asn	Val 390	Gln										
<2 <2 <2 <2	10> 11> 12> 13> 20> 21>	2717 DNA Homo	7 Sap	oiens	3										
	22>		2	(545)											
< 4	<00	8													
cagggtaa ccgcgcgc		ato	gago	cac	ggg	g aaq	g gga	acc	e gad	ato	g ct	c cc	ggaq		60 110
gcc gcc Ala Ala 15															158
gtg agc Val Ser 30															206
ctc aca Leu Thr															254
gge tee	ggc	tac	cgc	tgc	att	cgc	atc	aac	cac	aag	atg	gac	ccc	atc	302

			-9-		
Gly Ser Gl	y Tyr Arg (65	ys Ile Arg	Ile Asn His 70	Lys Met Asp Pro Ile 75	
atc agc ag Ile Ser Ar	g Val Ala S	gc cag atc er Gln Ile 85	gga ctc agc Gly Leu Ser	cag ccc cag ctg cac Gln Pro Gln Leu His 90	350
				gac ccc tat gag gtg Asp Pro Tyr Glu Val 105	398
	g Ile Gly G			gtc ttg tac gag gag Val Leu Tyr Glu Glu 125	446
gcc cca cto Ala Pro Leo	g gee gee t u Ala Ala S 130	cc tgt ggg er Cys Gly	ctc ctc acc Leu Leu Thr 135	tgc aag aac caa gtg Cys Lys Asn Gln Val 140	494
		er Pro Ser		gtg atg gca gtc tcc Val Met Ala Val Ser 155	542
caacagocca atatattat aatcettcaa cgtgcttgag ctagccaagg agcaaggtta acagttcaga tcagggcat atgtgtggc catggggat tatgtgtggc catggggat tgctgcatg tgctgcatg tgctgcatg tgctgcatg tgctgcatg tgctgcatc tctttgaaat agcagtattc tcttgaagat tgctgcatc cccctggg tatgtgcat cccctggg tatgtgcttag gcatgattat cctcctca agcagatca tgtggact tgtgagact cccctggg tgtgccc aaacgactca tgtattgccc acagaccag ccgatca ccaaaccac tgtattgcct ccaagccagtc ccaagcagtc ccaagcagtc ccaagcagtc ccaagcagtc ccaagcagtc ccaagcagtc ccaagcagtc ccaagcagtc ccaagaccagtc ccaagaccagtc cccaagaccagtc cccaagaccagtc cccaagaccagagc	cacatacot ttttttaag gggagotget tctgtgagoc agaagtggga gcaactgtga gcactgtga gcactgtga catgactga gggcagag catgactgt tcaagagtgga catgactgt tcaagagtgga catgactgt ctaagaggga atacttttag agagctaccg cccaggaggg atactaaat ttgggtaag agacatct tttggctgaa ggaacatct tttggctgaa gacactaat tgggaagg accttaagagg accttaagagg cctttaagaag cctttaagagg cctttaagagg cctttactg tcaccagacct tcagaaggt tactgagga cctttcatg tcaccagacct tcagaaggt tcaccagacct tcagaaggt tcactagagg cctttctg tcaccagacct tcagaaggt tcactagcagg tcactaggagg tcactacc tcagaaggt tcactagcagg tcactaggagg tcactaggagg tcactaggagg tcactagg tcaccagacct tcagaagg tcactaggagg tcactagg tcaccagacct tcagaagg tcactagg tcaccagacct tcagaagg tcactagg tcaccagacct tcagaagg tcaccagacct tcaccagaccag	caacctgggg aaggggaa tggaagtggc agggtcttggc acagaagggt tcocccaagcc acttaacaa tgaaaggcc tctaattct gggtttttgg tcaacactctc taaccact tcaacactctc tatttctag tctggaggaa tcctgctct tgggagaatg gacattgatg gacagggcta tcttcacc acttctccc tctttctag tctggagaa tcgttgtctg tggaagagtg tcttcacc gatttctag tctgctgtct tggagaatg tcttcacc tctttctacc tctgttctt tgcgcag tcctgcttct tgcgcag tcctccc tctttcacc tctttcacc tcgctgtct tgcacc tctgctct tgcgaagct tctcacc tctgctcc tctgccac tcccc tctccc tctccc tctcccc tctccc tctcccc tctccc tctccc tcccc tccc t	aactgtattt aagaaacca acccaaggt tataggaggg tagcaaccca cgggatttgc cactatgtta tocctagtt acctcaggg agggggaga accttgctt gcaatgaatt ccttttggaa aaaagctaca cctcaggtaactcacatgta toctcatgtt ccttttggaa aaagctaca cctcagtaca cctcagtaca acctagctac tctcagtaca acctggctact cctggatgcac tctcagtaca aaggggcct cggcaatttg cacttgctctct tctgtcaatt gcacttcctct tctgttaatgctt tttattgctt ggtgaaaca tccctgctctt tttattgctt tttattgctt tttattgctt tttattgctt tttattgatg tctcctctt	teat getgecgtga ttaaatgaag agctatttat aagttitttt taagaaaaaa gectttggag agaactgttg ggagetgta gggggtagac ggaagatgtg agaggaggac ectggggag gaaagagggc atcoctgget cetetattac tetttett tattiteta ectactgtec taagetgetg gecgtgaag gigggtagac gecgtgaag gtgggttattg gectgtagat gttgettec gagggaactg gaggttattg tttgggaccc aaagagtate cacatagac gttgetttagtg tttgggaaccc aggteettat eccacatgaa gtettgatg ggaactca ggteettat eccacatgaa tttgatg ggaactca ggteettta eccacatgaa tttgatg gaaaccca ggteettta eccacatgaac ttcecttetg etagaccat gtgcaatatg eagaactca gtgcaatatg eagaactca gtgcaatatg eagaactca gtgcaatatg eagaactca gtgcaatatg eagaactca gtgcaatatg eagaactca gtgcaatatg eagaagact ettggtatt tgcaagact ettggtatt egcaagact gtgcaact accagattet eccacattg accacaagt ettceccc ttgcacacagg tetcecca ttgatcaaa ggtgctatt taaagtcaa tetceccacatt taaagtcaa tetceccagg tttagaagca gectcatggt ttcactttaa aacaacaaa aagtaaaaat aaatagtagt accatattgt taatatgtt	595 5715 5775 5785 5795 5795 5795 5795 5795 579

<210> 9 <211> 157 <212> PRT <213> Homo Sapiens <400> 9 Met Ser His Gly Lys Gly Thr Asp Met Leu Pro Glu Ile Ala Ala Ala 10 Val Gly Phe Leu Ser Ser Leu Leu Arg Thr Arg Gly Cys Val Ser Glu 25 Gln Arg Leu Lys Val Phe Ser Gly Ala Leu Gln Glu Ala Leu Thr Glu 40 His Tyr Lys His His Trp Phe Pro Glu Lys Pro Ser Lys Gly Ser Gly 5.5 Tyr Arg Cys Ile Arg Ile Asn His Lys Met Asp Pro Ile Ile Ser Arg 70 75 Val Ala Ser Gln Ile Gly Leu Ser Gln Pro Gln Leu His Gln Leu Leu 90 Pro Ser Glu Leu Thr Leu Trp Val Asp Pro Tyr Glu Val Ser Tyr Arg 100 105 110 Ile Gly Glu Asp Gly Ser Ile Cys Val Leu Tyr Glu Glu Ala Pro Leu 120 125 Ala Ala Ser Cys Gly Leu Leu Thr Cys Lys Asn Gln Val Leu Leu Gly 135 140 Arg Ser Ser Pro Ser Lys Asn Tyr Val Met Ala Val Ser 145 150 <210> 10 <211> 1746 <212> DNA <213> Homo Sapiens <220> <221> CDS <222> (60)...(1037) <223> TIS11d <400> 10 gagectgact teagegetee cactetegge egacacecet catggecaac egttacace 59 atg gat ctg act gcc atc tac gag agc ctc ctg tcg ctg agc cct gac 107 Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu Leu Ser Leu Ser Pro Asp 1 gtg ccc gtg cca tcc gac cat gga ggg act gag tcc agc cca ggc tgg Val Pro Val Pro Ser Asp His Gly Gly Thr Glu Ser Ser Pro Gly Trp 20 gge tee teg gga eec tgg age etg age eec tee gae tee age eeg tet 203 Gly Ser Ser Gly Pro Trp Ser Leu Ser Pro Ser Asp Ser Ser Pro Ser 35 ggg gtc acc tcc cgc ctg cct ggc cgc tcc acc agc cta gtg gag ggc Gly Val Thr Ser Arg Leu Pro Gly Arg Ser Thr Ser Leu Val Glu Gly 50 ege age tgt gge tgg gtg eee eea eee eet gge tte gea eeg etg get 299 Arg Ser Cys Gly Trp Val Pro Pro Pro Pro Gly Phe Ala Pro Leu Ala 65 7.0 75 ccc ege etg gge eet gag etg tea eee tea eee aet teg eee aet gea 347 Pro Arg Leu Gly Pro Glu Leu Ser Pro Ser Pro Thr Ser Pro Thr Ala

-11-85 90 95

	85		90	95	
acc tcc acc acc Thr Ser Thr Thr 100	Pro Ser Ar				
tca gag agt ggg Ser Glu Ser Gly 115					
ggc ctg ggc gag Gly Leu Gly Glu 130		n Ala Asn A			
gaa ctc tgt cac Glu Leu Cys His 145					
cgc tgc cac ttc Arg Cys His Phe		n Pro Ser G			
cac cct cct gtg His Pro Pro Val 180	Leu Arg Gl				
ggc cgc cgg acc Gly Arg Arg Thr 195					
tcc tcc agc tcc Ser Ser Ser Ser 210	ttc tcg cc Phe Ser Pr 21	o Ser Ser S	Ser Pro Pro 220	cca cct ggg Pro Pro Gly	gac 731 Asp
ctt cca ctg tca Leu Pro Leu Ser 225					
gct cga aga gac Ala Arg Arg Asp		o Val Cys C			
act cct atc ago Thr Pro Ile Ser 260	Val Trp Gl				
tot gta cag too Ser Val Gln Ser 275					
agc agc ctg ggg Ser Ser Leu Gly 290		p Ser Pro V			
gca cca ccc cag Ala Pro Pro Gln 305					
cgc atc tct gtt Arg Ile Ser Val		acaaagtg ac	ctgeeeggt ca	gatcagct	1067

ggateteage ggggageeae gtetettgea etgtggtete tgeatggaee eeagggetgt ggggacttgg gggacagtaa tcaagtaatc cccttttcca gaatgcatta acccactccc etgaceteae getggggeag gtececaagt gtgeaagete agtatteatg atggtggggg atggagtgtc ttccgaggtt cttgggggaa aaaaaattgt agcatattta agggaggcaa tgaaccetet ecceacete tteeetgeee aaatetgtet ectagaatet tatgtgetgt gaataatagg cottcactgc coctcoagtt tttatagacc tgaggttcca gtgtctcctg gtaactggaa cototootga gggggaatoo tggtgotoaa attaccotoo aaaagcaagt 1487 agccaaagcc gttgccaaac cccacccata aatcaatggg ccctttattt atgacgactt 1547 tatttattct aatatgattt tatagtattt atatatattg ggtcgtctgc ttcccttgta tttttcttcc tttttttgta atattgaaaa cgacgatata attattataa gtagactata atatatttag taatatata tattacetta aaagtetatt titigtigtitt gggcattitt 1727 aaataaacaa totgagtgt 1746

<210> 11

<211> 326 <212> PRT

<213> Homo Sapiens

<400> 11

Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu Leu Ser Leu Ser Pro Asp 10 Val Pro Val Pro Ser Asp His Gly Gly Thr Glu Ser Ser Pro Gly Trp 20 25 30 Gly Ser Ser Gly Pro Trp Ser Leu Ser Pro Ser Asp Ser Ser Pro Ser 40 45 Gly Val Thr Ser Arg Leu Pro Gly Arg Ser Thr Ser Leu Val Glu Gly 50 55 60 Arg Ser Cys Gly Trp Val Pro Pro Pro Pro Gly Phe Ala Pro Leu Ala 70 75 80 Pro Arg Leu Gly Pro Glu Leu Ser Pro Ser Pro Thr Ser Pro Thr Ala 85 90 Thr Ser Thr Thr Pro Ser Arg Tyr Lys Thr Glu Leu Cys Arg Thr Phe Ser Glu Ser Gly Arg Cys Arg Tyr Gly Ala Lys Cys Gln Phe Ala His 120 125 Gly Leu Gly Glu Leu Arg Gln Ala Asn Arg His Pro Lys Tyr Lys Thr 135 140 Glu Leu Cys His Lys Phe Tyr Leu Gln Gly Arg Cys Pro Tyr Gly Ser 155 150 145 Arq Cys His Phe Ile His Asn Pro Ser Glu Asp Leu Ala Ala Pro Gly 175 165 His Pro Pro Val Leu Arg Gln Ser Ile Ser Phe Ser Gly Leu Pro Ser 185 180 Gly Arg Arg Thr Ser Pro Pro Pro Pro Gly Leu Ala Gly Pro Ser Leu 200 205 Ser Ser Ser Ser Phe Ser Pro Ser Ser Ser Pro Pro Pro Pro Gly Asp 215 220 210 Leu Pro Leu Ser Pro Ser Ala Phe Ser Ala Ala Pro Gly Thr Pro Leu 230 235 Ala Arq Arg Asp Pro Thr Pro Val Cys Cys Pro Ser Cys Arg Arg Ala 245 Thr Pro Ile Ser Val Trp Gly Pro Leu Gly Gly Leu Val Arg Thr Pro 260 265 Val Gln Ser Leu Gly Ser Asp Pro Asp Glu Tyr Ala Ser Ser Gly 275 280 Ser Ser Leu Gly Gly Ser Asp Ser Pro Val Phe Glu Ala Gly Val Phe 290 295 300 Ala Pro Pro Gln Pro Val Ala Ala Pro Arg Arg Leu Pro Ile Phe Asn 310 315 Arg Ile Ser Val Ser Glu

<210> 12 <211> 878

<212> DNA <213> Mus Musculus

325

<220>

<221> CDS

<222> (20)...(841)

<400> 12

ggg cag coc aat gtc toc tgc gcg tgc aac tgc cag cgc tct ttg ttc 100 Gly Gln Pro Asn Val Ser Cys Ala Cys Asn Cys Gln Arg Ser Leu Phe 15 20 25

ccc agc atg gag atc acg gag ctg gag ttc gtg caa atc gtg gtc atc Pro Ser Met Glu Ile Thr Glu Leu Glu Phe Val Gln Ile Val Val Ile $_{30}^{\rm M}$

196

628

gtg gta gtg atg atg gtg atg gtt atg att acg tgc ctg ctg agc Val Val Nal Met Wal Met Val Val Met Ile Thr Cys Leu Leu Ser 45 50

cac tac aag ctg tca gcc cgc tcc ttc atc agc cga cac agc cag gcc 244 His Tyr Lys Leu Ser Ala Arg Ser Phe Ile Ser Arg His Ser Gln Ala 60 70 75

agg agg agg aga gat gga ctg tcc tcg gaa gga tgc ctc tgg ccc tca Arg Arg Arg Asp Asp Gly Leu Ser Ser Glu Gly Cys Leu Trp Pro Ser 85 90 90

gag agt acg gtg tca ggt gga atg ccg gag cca cag gtc tat gcc ccg
Glu Ser Thr Val Ser Gly Gly Met Pro Glu Pro Gln Val Tyr Ala Pro
95 100 105

cct cgg ccc act gac cga ctc gct gtg ccc ccc ttc atc cag cgg agc
Pro Arg Pro Thr Asp Arg Leu Ala Val Pro Pro Phe Ile Gln Arg Ser
115 110 120

cga ttc caa ccc acc tac ccc tac ctg cag cac gaa att gcc ctg cca
Arg Phe Gln Pro Thr Tyr Pro Tyr Leu Gln His Glu Ile Ala Leu Pro
125
130
135

ccc acc atc tca ctg tct gat ggg gag gag ccc cca ccc tac cag ggc 484 Pro Thr Ile Ser Leu Ser Asp Gly Glu Glu Pro Pro Pro Tyr Gln Gly 140 150 155

coc tgc acc ctc cag cta cgg gac cct gag caa cag ctg gag ctg aac
Pro Cys Thr Leu Gln Leu Arg Asp Pro Glu Gln Gln Leu Glu Leu Asn
160 165 170

cgg gaa tot gtg cgc gca ccc cct aac cgg acc atc ttc gac agt gac 580 Arg Glu Ser Wal Arg Ala Pro Pro Asn Arg Thr Ile Phe Asp Ser Asp 175 180 185

ett ata gac age ace atg etg ggg gge eee tgt eee eee age agt aac

									14-							
Leu	Ile	Asp 190	Ser	Thr	Met	Leu	Gly 195	Gly	Pro	Cys	Pro	Pro 200	Ser	Ser	Asn	
tcg Ser	ggc Gly 205	atc Ile	agc Ser	gcc Ala	acc Thr	tgc Cys 210	tac Tyr	agc Ser	agc Ser	ggt Gly	ggg Gly 215	cgc Arg	atg Met	gag Glu	ggg ggg	676
ccg Pro 220	ccc Pro	ccc Pro	acc Thr	tac Tyr	agc Ser 225	gag Glu	gtc Val	att Ile	ggc Gly	cac His 230	tac Tyr	cct Pro	ggc Gly	tcc Ser	tcc Ser 235	724
ttc Phe	cag Gln	cac His	cag Gln	caa Gln 240	agt Ser	aac Asn	ggg Gly	cca Pro	tcc Ser 245	tcc Ser	ctg Leu	cta Leu	gag Glu	ggg Gly 250	acc Thr	772
egg Arg	ctc Leu	cat His	cac His 255	tcg Ser	cac His	att Ile	gcc Ala	cca Pro 260	ctg Leu	gag Glu	aac Asn	aag Lys	gag Glu 265	aag Lys	gag Glu	820
					ccc Pro		tago	gagto	ggg (ggee	gggg	eg co	etgta	aggca	a	871
aaac	ege															878
	<:	210> 211> 212> 213>	274 PRT	Mus	culu	s										
Mot	< 0.1 vz	400>	13 Aen	Glv	Thr	Ala	Ala	Ala	Ala	Ala	Glv	Gln	Pro	Asn	Val	
1	_			5					10					15 Glu		
	-		20					25					30	Met		
		35					40					45				
	50					55					60			Leu		
Ala 65	Arg	Ser	Phe	Ile	Ser	Arg	His	Ser	Gln	Ala 75	Arg	Arg	Arg	Asp	Asp 80	
Gly	Leu	Ser	Ser	Glu 85		Cys	Leu	Trp	Pro	Ser	Glu	Ser	Thr	Val 95	Ser	
Gly	Gly	Met		Glu	Pro	Gln	Val	Tyr 105	Ala	Pro	Pro	Arg	Pro	Thr	Asp	
Arg	Leu	Ala	100 Val	Pro	Pro	Phe	Ile	Gln	Arg	Ser	Arg	Phe 125	Gln		Thr	
Tyr			Leu	Gln	His				Leu	Pro	Pro	Thr		Ser	Leu	
Ser	130 Asp	Gly	Glu	Glu	Pro	135 Pro		Tyr	Glr	Gly	140 Pro		Thr	Leu	Gln	
145 Leu		Asp	Pro	Glu	150 Gln		Leu	Glu	Let	155 Asn		Glu	Ser	Val	160 Arg	
				165	5				170	1			Asp	175 Ser	Thr	
			180	1				185	i				190)	Ala	
		195	;				200	1				205	5		Tyr	
	210) _				215	i i				220)			Gln	
Ser 225		ı val	. TT6	: 617	230) · TĀI	. FIC	. 017	261	235	5	. 011	. 113.6	. 021	240	

```
Ser Asn Gly Pro Ser Ser Leu Leu Glu Gly Thr Arg Leu His His Ser
                                    250
                245
His Ile Ala Pro Leu Glu Asn Lys Glu Lys Glu Lys Gln Lys Gly His
                                265
Pro Leu
      <210> 14
      <211> 693
      <212> DNA
      <213> Homo Sapiens
      <220>
      <221> unsure
      <222> (639)...(639)
      <223> a, c, q, or t/u
      <400> 14
tttttttgca agetetetta gettgtgcat teagaceaga eateaeatgt aaatatttat
acacaggag gtgggagggg agggccacac gatgcgttgc tgcgcccccc gccttcctct
                                                                       120
cacteetett etaagaageg eggagtgtte tgeettttea eetaegeage eecageeegg
                                                                       180
ccccctggg gaccctagag agggtgtcct tictgtttat ccttctcttt gctccagatg
                                                                       240
getgegetet etaggggege gatgtgtgtg tgggggaace eggteeceet ecagcaagga
gggcggccca ctgctctgct ggtgctggaa ggaggacccc gggtagtggc cgatgacctc
getgtaggtg ggeggeggee cetecatgeg ceegeegetg cegtageaeg tggegetgat
geoogagtta etgetggggg ggeaggggee geecageetg geactateea teaggteact
gtogaagatg gttotgtttg ggggtgegeg caccgactee eggtteagtt ccagetgetg
                                                                       540
ctcggggtcc cgaagctgga gggtgcaggg gccctggtag ggtgggggctc ctcccgtctg
                                                                       600
acaqcgagat ggtgggcggc agtcgatctc gtgctgcang tacggatagg tgggctggaa
                                                                       660
                                                                       693
geggtggaag cgctcccgct gggcgaaagg cgg
      <210> 15
      <211> 475
      <212> DNA
      <213> Mus Musculus
      <400> 15
aattegtega catggettga tgggggteaa eggeacegee geegeegeeg eegggeagee
caatgtotee tgegegtgea actgeeageg etetttgtte eecageatgg agateaegga
                                                                       120
getggagtte gtgcaaateg tggtcategt ggtagtgatg atggtgatgg tggttatgat
                                                                       180
tacqtgcctg ctgagccact acaagctgtc agcccgctcc ttcatcagcc gacacagcca
                                                                       240
ggecaggagg agagacgatg gactgtcctc ggaaggatgc ctctggccct cagagagtac
ggtgtcaggt ggaatgccgg agccacaggt ctatgccccg cctcggccca ctgaccgact
                                                                       360
egetgtgece ecetteatee ageggageeg attecaacee acetaceeet acetgeagea
                                                                       420
cgaaattgcc ctgccaccca ccatctcact gtctgatggg gaggagcccc caccc
                                                                       475
       <210> 16
       <211> 8093
       <212> DNA
       <213> Homo Sapiens
       <220>
       <221> unsure
       <222> (6477) ... (6477)
       <223> c or t/u
       <221> unsure
       <222> (6837)...(6837)
       <223> a or c
       <400> 16
```

ctcagctccc	tgtggtgggg	gatggcagag	gcttcccgct	ccccgcagct	ggtttgcaca	60
gcctcccgac	tgtgccgtgg	tgtctccttc	cctaaagtgg	gacagtcgtt	tctgtgtcct	120
getggeetet	gaggaacaga	cgtgtgtgag	aggccttcag	ggcctgatgg	ctggggtggt	180
gacagtgcct	ggagaatggg	tggggactgg	aggggccagg	tggctaacca	ctctcctctt	240
ccatggcage	ggagctggag	ttcqcccaaa	tcatcatcat	cgtcgtggtg	gtcacggtga	300
taataataat	catcgtctgc	ctgctgaacc	actacaaagt	ctccacgcgg	tccttcatca	360
accoccoaa	ccagagccgg	aggcgggagg	acagactacc	gcaggaaggg	tacctatage	420
cttcagacag	cgccgcaccg	caactaaaca	cctcggagat	catgcatgcc	ccgcggtcca	480
	cacagegeeg					540
cctaccccta	tgtgcagcac	gagattgatc	ttcctcccac	catctccctd	tecgaeggtg	600
220000000	tccttaccag	gagacegace	ccctacaact	ccadagaccet	gaacagcaga	660
tagagecace	ccgagagtcc	atasaaaccc	cacccaaccc	aaccatattt	gacagtgatt	720
tygaactcaa	tgctatgtat	gegagggeee	cateceaaceg	caccaccacc	tcaaacetce	780
caacayacac	ctgcagcagt	agegggggee	tagaaaaaa	accccccaca	tacacccacc	840
gugcaageae	cigcagcagi	aacyggagga	tagatagagac	accccccaca	acagegagg	900
	ccacccagge					960
geageagaet	gcagtttcag	cagaacaarg	Cagagagcac	aatagtaccc	accaaaggca	1020
aagataggaa	gcctgggaac	ctggtctgat	teetteeaac	gtgcacttca	gctggagaaa	
gaaaccaaga	agggaagcgg	cegetgggee	cctcctgcgc	acagtgttgt	teagttteae	1080
atggtacaaa	taagtaaaac	caaatgagca	aacacggtct	ttgtttctga	ttccttttag	1140
gggaattgca	tgcaaactag	actgaaatga	tacaaacttc	catctggtct	gaccgcaaac	1200
	tggggacagg					1260
gatgctttga	agataccatg	aaataaaacc	cacagaggta	tttgatgtat	ttaattgtga	1320
	tgcagataaa					1380
aaggaagcat	tattatatat	tattgtgggg	aagaaccagc	cagttcgctt	tttctcctaa	1440
ggtgtggact	tttattttgt	tttaaaaata	tgaatcaaaa	ttcctgtgtt	gtgtgccaag	1500
gtataaagtg	gagaagttag	atgagtgcaa	ggagctcctt	tgtgttgtga	tgatgtgttt	1560
taaaagttgc	actatcttaa	tgttgaaaat	atttacaagg	gaactgtttt	acgtgaagtt	1620
	tcttttcacc					1680
	atccaagaaa					1740
	aagtcattat					1800
gettttggag	acttttggat	ggaagataag	atagggaaga	ttaagttcca	gcatttctga	1860
cttottattt	tgagttactc	toctactett	aggetgeata	gtttatgaga	aaatqaacac	1920
atgratttat	ggatccagta	tcatgcagtg	ctgccctcat	cetecadead	tocaatttct	1980
	agatttttt					2040
	ttgtttaaaa					2100
	ttcccattgc					2160
actactcaat	tcacaggagg	ctcccagcag	ccaccccaca	tecageetae	acagaacttt	2220
catatagaaa	tggtgtgggt	aataattttc	ttatgctttg	gaagggggta	gaaataatga	2280
canagagaga	ccatgttgct	gatcataata	ataagccatt	gtgggttatt	gtatgtcact	2340
	tagcattctt					2400
	aaacccttcc					2460
ggaccccacc	gagggggcaa	atasetassa	aggagggg	aggoadgado	acatocaott	2520
gagaacagcg	ctagaaaact	gegacegaag	attattaatt	ttaatatttc	ctcatattta	2580
aaaatycaaa	ttcttatata	aactctaaac	actgccagtc	ttctccacat	ataaacacta	2640
	gagcagcagc					2700
						2760
	ctctgccatg					2820
	atgattccat					2880
tgtgtttgtg	tetgtetgtg	ggtetegaag	grgareegre	ggtgeggtgg	tecchiques	2940
taactggaga	gactgttcca	aaccccaaga	gttgtctgat	cctagtetgt	tecettetge	3000
	tgtagatagg					3060
	atcctttgca					3120
gagaggaaaa	acacaggcac	cagttgtcag	ctcatgctta	caacctgtgt	ggaagtatat	
acagttgaga	gtcacagtgg	aggttctgag	actggattca	gtcttgttcc	agtgacagtt	3180
	tgctggagag					3240
	aaccctggag					3300
	ggcaaagatg					3360
	cttggtcagg					3420
tttcagttct	cacctgcagt	tttggtgaag	caggagatgc	accccacage	tctagctctc	3480
aaatggcttc	acagteetta	cttctctacc	tgcctcaaga	aggggctcag	agcagagact	3540
tgtgaattcc	ttagtaactg	tgagtatatg	aatgtgttgc	acatgtccac	agtattggcg	3600
	ataattcaga					3660
	-					

```
aaccacccta gagaactgcc tttgttaaat agttatttaa agactcatac atatcaaacc
                                                                     3720
atgactttga aaggtcttcg aggctggggc tctgtaatga attagtttaa aagccaaggt
                                                                     3780
                                                                     3840
cataacatga attgatggtc aatttccctt cagcagaagg aaaaggtgat ttagatcagt
agotottttg aaggttgtgg ctgacctgtt cataccgtgt cgcctcatgg ctagtgtggc
                                                                     3900
                                                                     3960
gttgaaagag tagcgactgg gaagatacaa cttacacagt ggggcctatt gttctttcaa
                                                                     4020
quaccetttt tttagettat agaacceatg ggtccagttt agtaacgagt gatttaggca
atcaatgata ggtttataat cttagattat tccagcaaag tgtggattgc attgttagga
                                                                     4080
                                                                     4140
agaacatttg gtgggaatga acactcotgg gcatacogct gacttttgtc ccttgttccc
ggtgtaggag acccaaggca tottgaatoo catotataag aacacaatot tocagcatac
                                                                     4200
gtttgctttt tcagaaactc tagcattctc tttaaatact gacgcaatcc ttaatggaaa
                                                                     4260
agagatttca tgaagcaaat tatgtatttc aatagttctt ctatttttag tgtccaaaat
                                                                     4320
ttactaatac agaagettga caageatgte etcaecetee ecaecacata aacacatgga
                                                                     4380
cacacaceca agccacaaga aatcccaaga gagcagaage gaatttttaa aagatttate
                                                                     4440
gtgaggactg catttccatt cactaatttt ggctcaaact tatgaggcag gaaatagggg
                                                                     4500
ccaacagtaa atgggggagg cctcctgaca ccagcagagg aattttgtac ccaggcgagg
                                                                     4560
acttettgaa ettetgegta teteegtttg atetetttea eetttattte atetteataa
                                                                     4620
gaatgagaaa ggotcaaaag gaagcacttt tagaaatott ototgacota gaagaatoca
                                                                     4680
tecaaatece tgeetteete tetgaaceaa eagtteeett etetgacagg gggeeateet
                                                                      4740
ctatottoca tocagoggot ottootttta ggaaggotot ggtgcagago acttcaaata
                                                                      4800
                                                                     4860
tgtcctcagg ccagatactg attgctagta gagagacacc cggcacccag tccgaagccc
teceteaaag gaceggetta tggegttggt caetggeagg eteagagaca ttetaetgtg
                                                                     4920
ggcgcaggga gcccggcccc ccatgcagcc atgactggat gcgcccccat ctcgggggct
                                                                      4980
tgctgcactg cttgtttatt gaattttgct acttagaatg gcaacattaa ctttgtgtac
                                                                     5040
cattcatttt ttaaaaattt tocaaagoto ggcagtgtat gaaagaaaaa actgggaaag
                                                                      5100
                                                                      5160
atacttggtt tctgttaact tttgtgttgc ttgcttaagt gattaaagcc agtgcttgga
gecaageett catgecacga acatgeteca cageetgeee tttgetetee tgeteacact
                                                                      5220
gaccaagaat gccgcgtgct tggcctactg aggtgaaagg acaattgaat gacaggtggg
                                                                      5280
caaagggaga acttcccctt cttggtgcga ggaaagtcac aaatttaaaa atgttgcttc
                                                                      5340
                                                                      5400
cageceagat cetaaatget agtteteage agetgegtgg ettacegtte gecatteea
ccaccgccag ctgccagcac cgctacagat cacagagatg tgaacagaca atggaaagca
                                                                      5460
ctcttagcct tgcagtggtc tacatttttt aggaaccaat atttcagcat tctttattac
                                                                      5520
coggcacgot gtgtcctttg cagagttcaa gtttatgtta ctgccagggt cagacagtca
                                                                      5580
tttgetgetg etgetgetge tetegaactg gatgeattag gaagetgetg
                                                                      5640
totgagtgta ggaatgtett getaagaaag caatgtette etteateett ttetttette
                                                                      5700
                                                                      5760
cetetgegtg teettgtttt tgtgtaatge gggagagggt tagagetata gagattatat
atacactate egtgeacatt atatatatgt agatatacee ctateatgte agagatetge
                                                                      5820
atgtcagttt ttcagcaact aaggtgcctc atgttctgag ttcagcagat ataggaacca
                                                                      5880
agcogococo tootgoactt gatgotocca cotttgttgt gootcactta aaatggtgot
                                                                      5940
tttttcagtt gtctgtcttt tcttatgttt ttatttgtaa ggtgctgtat ataagttgaa
                                                                      6000
tatattatgc acatatccta cccaatgggt agaacaaaaa gttgttaata ctgtaatata
                                                                      6060
 atgtatagat gataccaatt ttaacagaaa tggcatagaa tttgtgaatg cctatgtgct
                                                                      6120
                                                                      6180
 ttgtcctctt ttgtaaggaa atttgcaaat ggatgcatac agattaaagt ctatgtagtt
                                                                      6240
 tattttccta ttaaatatca atattataac acaagagaaa gaagtgtgaa caaacaagca
 acagtttatg accagcgtat atatagcaat ggaaagttgc atctttgctg tgaaaacact
                                                                      6300
 ttaaagaaaa tacttttaa aaaatcccac agctttttgg ttgccactag acgcttctta
                                                                      6360
                                                                      6420
 ttttaatcat tttagtaatg ctcagctgga ccagtgttag ttatatttga gtcagaaaaa
 tgttgttttt caacttgctt tataatctcc tgcatctatc tcctgctgta gcatcaygaa
                                                                      6480
                                                                      6540
 ggtgtcaggc aacagtgaaa agtgcacatt tttgttgttg cagaaactgt gtcagaggaa
 taagtaaatc agcctgcagc agaagacttt gttcagctcc agaggcatct gtgaccgtct
                                                                      6600
 gtgtccaagt ctctctgtgc ctttttcttt tacaaactga agctgtggag ccaatgaagt
                                                                      6660
                                                                       6720
 aacagtagag attgtaggga aagaatacct caggaaaaac aaatacactt acaagaagac
                                                                       6780
 cctgttctta gaaaatgtgt ttagttatgg gttagcacta gaagagactt ggctgtcagc
 caqccaagtg aaggacetet catecattee catteatgte ceateataat aeggacmeaa
                                                                       6840
 aaagcaaact cggttttgcc atcagttaga aattacgttt tggattgtat attgttacat
                                                                       6900
 ctctcttcca gcttagtttt tagtgtctga ttgtgacctc tgcatttatc ttcaaatacc
                                                                       6960
                                                                       7020
 ctaattttaa aacaaagaa caagaaaagt ttataacacc atgttcacta aaaccacggt
 tgaatettgg gtgtgggcat cetttegagt gttgtecata agageagtte gtggaatttt
                                                                       7080
                                                                       7140
 geccatetga eccatattat cagettatte tgecaecaga gtagagteta ataaatteea
 aagtttttat ttgctccatg gtgtatgttc tgactttgaa aatgtcagat tctataatca
                                                                       7200
                                                                       7260
 tacccctaac atccaggaga caaatgacag attatcttta aactgaaatt gactctacaa
 tgcaaccett aatgetgaat ggattaaaaa agtcageeet tttagtatet gtttgaaagg
                                                                      7320
```

geogtaaaaa gttgacaett ttgttgttgt ggateetgeg tgtetagaee caegtgttgt 7380 ttccatcgta tactgtaggg tgcacccctt gggattcatc attaagaact gaggctcact 7440 gttgtcagaa acaaagctcc cacccccag gttcaacctt gtgggagaac tgttgagcat 7500 7560 gagaatgtte tagacteaga ggtactaaaa tttgttacca catcattget teetttetae aggacqaatt qaggcttaaa ctttactgtt aatgatactg gttcatttta atgtgcttgt 7620 7680 tggtatgttg ctatttttca tttcatagct ttcaaaaaatc atgctaattg tatacttgtc tagtttaagg ctattttaaa atatgtacaa tactattcac agcatttagt togtttaatt 7740 tttattataa agcaatctac taaaaaagta caactgtatt tgaacttttc aatagttgtt 7800 tgtgagctat gataatcaaa agtcattaaa gtctttttta acaaacattc gtgcttactt 7860 ttcaacataa ttcccagtta tatacagaaa aagatttcca cctgtcacgt atctgcctct 7920 tttacctgag caatggtgta gttcttagac ctaaggtctg taattgcaat acttttaaag 7980 aaagatgttg ctctaagtgc tgtttgttag ttatgaaatc agatttttct gcttgttctt 8040 8093 aatgetgtgg teaaaceata geacaaaate attaaaaata ateageggea tac

```
<210> 17
<211> 513
<212> DNA
<213> Homo Sapiens
<220>
<221> unsure
<222> (8)...(9)
<223> a, c, g, or t/u
<221> unsure
<222> (28)...(28)
<223> a, c, g, or t/u
<221> unsure
<222> (34)...(34)
<223> a, c, g, or t/u
<221> unsure
<222> (42)...(42)
<223> a, c, g, or t/u
<221> unsure
<222> (44)...(44)
<223> a, c, g, or t/u
<221> unsure
<222> (46)...(46)
<223> a, c, g, or t/u
<221> unsure
<222> (49)...(49)
<223> a, c, g, or t/u
<221> unsure
<222> (53)...(53)
<223> a, c, g, or t/u
<221> unsure
<222> (55)...(55)
<223> a, c, q, or t/u
<221> unsure
<222> (66)...(66)
<223> a, c, g, or t/u
```

60

120

180

240

300

360

420

480 513

<221> unsure <222> (410)...(410) <223> a, c, g, or t/u

<400> 17

aggggganna gagctgatec ttgtatanct gacnactttg cnananacne aanangaaga ggaagnageg coggtgcaca cacaccagag cgtttegece atttgaacet ttacetcett agccagattget tgaatcagtg atttatggea tateatecge cttggggacat tttetcegact atcetgttat teacetgtga actgggacat caataatgat gggetcacta gateagggagaagagaagact gcatacaaat aaatgegtaa aageactgat taacctatga cacgtgctgg attggtagag cggatetgga catgatgat atactatge ggtctacata ggtctgcagg cgactotgga cctgaacgag tateatagcg agccgagcan cetagcctgctgtgatgga acgtgtagat acgagcagaa cttgatgaag cccgaagggg ctggtcacat ggstgatcaca gotgtgacag gacaccaca cac